

# SCORE Search Results Details for Application 10553669 and Search Result 20071121\_092707\_us-10-553-669-1.rag.

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OM protein - protein search, using sw model

Run on: November 21, 2007, 09:27:44 ; Search time 121 Seconds  
(without alignments)  
1393.680 Million cell updates/sec

Title: US-10-553-669-1  
Perfect score: 1842  
Sequence: 1 MKRASAGGSRLLAWLWLQA.....TDEEPLGLPKCCQPDAAADKA 344

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2782304 seqs, 489333398 residues

Total number of hits satisfying chosen parameters: 2782304

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_200701:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*  
9: geneseqp2005s:\*  
10: geneseqp2006s:\*  
11: geneseqp2007s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
------------	-------	-------------	--------	----	-------------

1	1842	100.0	344	8	ADM33974	Adm33974	Human	Nog
2	1842	100.0	344	8	ADU21101	Adu21101	Human	Nog
3	1842	100.0	344	9	ADY34440	Ady34440	Human	Nog
4	1842	100.0	344	9	AEB19597	Aeb19597	Human	Nog
5	1842	100.0	344	9	AEB86619	Aeb86619	Human	NOG
6	1842	100.0	472	3	AAB33426	Aab33426	Human	PRO
7	1842	100.0	473	2	AAy41745	Aay41745	Human	PRO
8	1842	100.0	473	3	AAB44301	Aab44301	Human	PRO
9	1842	100.0	473	3	AAB24410	Aab24410	Human	PRO
10	1842	100.0	473	3	AAy95345	Aay95345	Human	PRO
11	1842	100.0	473	4	AAU12362	Aau12362	Human	PRO
12	1842	100.0	473	4	AAU04589	Aau04589	Human	Nog
13	1842	100.0	473	4	AAB49891	Aab49891	Human	PRO
14	1842	100.0	473	4	AAB50908	Aab50908	Human	PRO
15	1842	100.0	473	5	AAU83655	Aau83655	Human	PRO
16	1842	100.0	473	5	AAO21479	Aao21479	Human	NgR
17	1842	100.0	473	5	ABB81081	Abb81081	Human	Nog
18	1842	100.0	473	5	ADY31868	Ady31868	Novel	hum
19	1842	100.0	473	6	ABO17806	Abol17806	Novel	hum
20	1842	100.0	473	6	ABU80802	Abu80802	Human	PRO
21	1842	100.0	473	6	ABO25247	Abo25247	Novel	hum
22	1842	100.0	473	6	ABO33768	Abo33768	Novel	hum
23	1842	100.0	473	6	ABU81060	Abu81060	Human	PRO
24	1842	100.0	473	6	ABU72253	Abu72253	Novel	hum
25	1842	100.0	473	6	ABU66760	Abu66760	Human	PRO
26	1842	100.0	473	6	ABU84933	Abu84933	Human	sec
27	1842	100.0	473	6	ABU59841	Abu59841	Novel	sec
28	1842	100.0	473	6	ABU61131	Abu61131	Human	PRO
29	1842	100.0	473	6	ABO25031	Abo25031	Human	sec
30	1842	100.0	473	6	ABU80400	Abu80400	Human	sec
31	1842	100.0	473	6	ABU82111	Abu82111	Novel	hum
32	1842	100.0	473	6	ABU67036	Abu67036	Human	sec
33	1842	100.0	473	6	ABR59665	Abr59665	Human	Nog
34	1842	100.0	473	6	ADA45901	Ada45901	Novel	hum
35	1842	100.0	473	6	ADA76332	Ada76332	Human	PRO
36	1842	100.0	473	6	ABJ72291	Abj72291	Human	PRO
37	1842	100.0	473	6	ADA18982	Ada18982	Human	PRO
38	1842	100.0	473	6	ADA61605	Ada61605	Homo sapi	
39	1842	100.0	473	6	ADB19390	Adb19390	Novel	hum
40	1842	100.0	473	6	ADB27931	Adb27931	Human	PRO
41	1842	100.0	473	6	ADA86410	Ada86410	Novel	hum
42	1842	100.0	473	6	ADB15974	Adb15974	Human	PRO
43	1842	100.0	473	6	ADA47760	Ada47760	Human	PRO
44	1842	100.0	473	6	ADA67555	Ada67555	Human	PRO
45	1842	100.0	473	6	ADB30562	Adb30562	Human	PRO

## ALIGNMENTS

## RESULT 1

ADM33974

ID ADM33974 standard; protein; 344 AA.

XX

AC ADM33974;

XX

DT 03-JUN-2004 (first entry)

XX

DE Human Nogo receptor-1 1-344 amino acid sequence SEQ ID NO:6.

XX

KW immunogenic; Nogo receptor-1; neuroprotective; nootropic; anticonvulsant;

KW antiparkinsonian; cerebroprotective; vasotropic; vulnerary; gene therapy;

KW multiple sclerosis; ALS; Huntington's disease; Alzheimer's disease;

KW Parkinson's disease; diabetic neuropathy; stroke; traumatic brain injury;

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OM protein - protein search, using sw model

Run on: November 21, 2007, 09:27:44 ; Search time 121 Seconds  
(without alignments)  
1393.680 Million cell updates/sec

Title: US-10-553-669-2  
Perfect score: 1838  
Sequence: 1 MKRASSGGSRLPTWVLWLQA.....TDEELLGLPKCCQPDAAADKA 344

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2782304 seqs, 489333398 residues

Total number of hits satisfying chosen parameters: 2782304

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_200701:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*  
9: geneseqp2005s:\*  
10: geneseqp2006s:\*  
11: geneseqp2007s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	Query					
No.	Score	Match	Length	DB	ID	Description

1	1838	100.0	344	8	ADM33976	Adm33976	Rat	Nogo
2	1838	100.0	344	8	ADU21102	Adu21102	Rat	Nogo
3	1838	100.0	344	9	ADY34442	Ady34442	Rat	Nogo
4	1838	100.0	344	9	AEB19599	Aeb19599	Rat	Nogo
5	1827.5	99.4	345	9	AEB86620	Aeb86620	Rat	NOGO
6	1816	98.8	471	10	AEH43954	Aeh43954	Rat	Ngr-1
7	1793	97.6	441	8	ADT77804	Adt77804	Chimeric	
8	1793	97.6	473	8	ADT77786	Adt77786	Rat	Nogo
9	1739	94.6	473	4	AAB87102	Aab87102	Mouse	sec
10	1739	94.6	473	4	AAU04590	Aau04590	Mouse	Nog
11	1739	94.6	473	5	AAO21488	Aao21488	Mouse	NgR
12	1739	94.6	473	5	AAE26454	Aae26454	Mouse	TAN
13	1739	94.6	473	5	ABB81082	Abb81082	Mouse	Nog
14	1739	94.6	473	6	ABR59666	Abr59666	Murine	No
15	1739	94.6	473	8	ADG75447	Adg75447	Mouse	NoG
16	1739	94.6	473	9	AEB19596	Aeb19596	Soluble	N
17	1739	94.6	473	10	AEK91090	Aek91090	Mouse	TAN
18	1736	94.5	473	4	AAB87169	Aab87169	Mouse	sec
19	1736	94.5	473	4	AAB87166	Aab87166	Mouse	sec
20	1735	94.4	473	4	AAB87167	Aab87167	Mouse	sec
21	1735	94.4	473	4	AAB87168	Aab87168	Mouse	sec
22	1702	92.6	319	9	AEB19608	Aeb19608	Rat	solub
23	1695	92.2	318	8	ADU21106	Adu21106	Rat	Nogo
24	1695	92.2	318	9	AEB86602	Aeb86602	Rat	NOGO
25	1654	90.0	310	8	ADM33977	Adm33977	Rat	Nogo
26	1654	90.0	310	9	ADY34443	Ady34443	Rat	Nogo
27	1654	90.0	310	9	AEB19600	Aeb19600	Rat	Nogo
28	1635	89.0	420	8	ADT77798	Adt77798	Chimeric	
29	1635	89.0	452	8	ADT77806	Adt77806	Chimeric	
30	1612	87.7	473	8	ADG75446	Adg75446	Macaque	b
31	1611	87.6	423	4	AAB87116	Aab87116	Mouse	TAN
32	1611	87.6	447	4	AAB87104	Aab87104	Mouse	mat
33	1605	87.3	344	8	ADM33974	Adm33974	Human	Nog
34	1605	87.3	344	8	ADU21101	Adu21101	Human	Nog
35	1605	87.3	344	9	ADY34440	Ady34440	Human	Nog
36	1605	87.3	344	9	AEB19597	Aeb19597	Human	Nog
37	1605	87.3	344	9	AEB86619	Aeb86619	Human	NOG
38	1605	87.3	472	3	AAB33426	Aab33426	Human	PRO
39	1605	87.3	473	2	AAY41745	Aay41745	Human	PRO
40	1605	87.3	473	3	AAB44301	Aab44301	Human	PRO
41	1605	87.3	473	3	AAB24410	Aab24410	Human	PRO
42	1605	87.3	473	3	AAY95345	Aay95345	Human	PRO
43	1605	87.3	473	4	AAU12362	Aau12362	Human	PRO
44	1605	87.3	473	4	AAU04589	Aau04589	Human	Nog
45	1605	87.3	473	4	AAB49891	Aab49891	Human	PRO

## ALIGNMENTS

## RESULT 1

## ADM33976

ID ADM33976 standard; protein; 344 AA.

XX

AC ADM33976;

XX

DT 03-JUN-2004 (first entry)

XX

DE Rat Nogo receptor-1 1-344 amino acid sequence SEQ ID NO:8.

XX

KW immunogenic; Nogo receptor-1; neuroprotective; nootropic; anticonvulsant;

KW antiparkinsonian; cerebroprotective; vasotropic; vulnerary; gene therapy;

KW multiple sclerosis; ALS; Huntington's disease; Alzheimer's disease;

KW Parkinson's disease; diabetic neuropathy; stroke; traumatic brain injury;

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OM protein - protein search, using sw model

Run on: November 21, 2007, 09:27:44 ; Search time 100 Seconds  
(without alignments)  
1393.680 Million cell updates/sec

Title: US-10-553-669-3  
Perfect score: 1515  
Sequence: 1 PCPGACVCYNEPKVTTSCPQ.....QRLAGRDLKRLAANDLQGCA 285

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2782304 seqs, 489333398 residues

Total number of hits satisfying chosen parameters: 2782304

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_200701:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*  
9: geneseqp2005s:\*  
10: geneseqp2006s:\*  
11: geneseqp2007s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
------------	-------	-------------	--------	-------	-------------

1	1515	100.0	285	8	ADU21103	Adu21103	Human	Nog
2	1515	100.0	285	9	AEB19607	Aeb19607	Human	sol
3	1515	100.0	285	9	AEB86599	Aeb86599	Human	NOG
4	1515	100.0	310	8	ADM33975	Adm33975	Human	Nog
5	1515	100.0	310	9	ADY34441	Ady34441	Human	Nog
6	1515	100.0	310	9	AEB19598	Aeb19598	Human	Nog
7	1515	100.0	319	8	ADU21104	Adu21104	Human	Nog
8	1515	100.0	319	9	AEB19606	Aeb19606	Human	sol
9	1515	100.0	319	9	AEB86600	Aeb86600	Human	NOG
10	1515	100.0	344	8	ADM33974	Adm33974	Human	Nog
11	1515	100.0	344	8	ADU21101	Adu21101	Human	Nog
12	1515	100.0	344	9	ADY34440	Ady34440	Human	Nog
13	1515	100.0	344	9	AEB19597	Aeb19597	Human	Nog
14	1515	100.0	344	9	AEB86619	Aeb86619	Human	NOG
15	1515	100.0	472	3	AAB33426	Aab33426	Human	PRO
16	1515	100.0	473	2	AAY41745	Aay41745	Human	PRO
17	1515	100.0	473	3	AAB44301	Aab44301	Human	PRO
18	1515	100.0	473	3	AAB24410	Aab24410	Human	PRO
19	1515	100.0	473	3	AAY95345	Aay95345	Human	PRO
20	1515	100.0	473	4	AAU12362	Aau12362	Human	PRO
21	1515	100.0	473	4	AAU04589	Aau04589	Human	Nog
22	1515	100.0	473	4	AAB49891	Aab49891	Human	PRO
23	1515	100.0	473	4	AAB50908	Aab50908	Human	PRO
24	1515	100.0	473	5	AAU83655	Aau83655	Human	PRO
25	1515	100.0	473	5	AAO21479	Aao21479	Human	NgR
26	1515	100.0	473	5	ABB81081	Abb81081	Human	Nog
27	1515	100.0	473	5	ADY31868	Ady31868	Novel	hum
28	1515	100.0	473	6	ABO17806	Abo17806	Novel	hum
29	1515	100.0	473	6	ABU80802	Abu80802	Human	PRO
30	1515	100.0	473	6	ABO25247	Abo25247	Novel	hum
31	1515	100.0	473	6	ABO33768	Abo33768	Novel	hum
32	1515	100.0	473	6	ABU81060	Abu81060	Human	PRO
33	1515	100.0	473	6	ABU72253	Abu72253	Novel	hum
34	1515	100.0	473	6	ABU66760	Abu66760	Human	PRO
35	1515	100.0	473	6	ABU84933	Abu84933	Human	sec
36	1515	100.0	473	6	ABU59841	Abu59841	Novel	sec
37	1515	100.0	473	6	ABU61131	Abu61131	Human	PRO
38	1515	100.0	473	6	ABO25031	Abo25031	Human	sec
39	1515	100.0	473	6	ABU80400	Abu80400	Human	sec
40	1515	100.0	473	6	ABU82111	Abu82111	Novel	hum
41	1515	100.0	473	6	ABU67036	Abu67036	Human	sec
42	1515	100.0	473	6	ABR59665	Abr59665	Human	Nog
43	1515	100.0	473	6	ADA45901	Ada45901	Novel	hum
44	1515	100.0	473	6	ADA76332	Ada76332	Human	PRO
45	1515	100.0	473	6	ABJ72291	Abj72291	Human	PRO

## ALIGNMENTS

RESULT 1  
ADU21103

ID ADU21103 standard; protein; 285 AA.  
 XX  
 AC ADU21103;  
 XX  
 DT 27-JAN-2005 (first entry)  
 XX  
 DE Human Nogo receptor NgR1 polypeptide fragment ( residues 26-310).  
 XX  
 KW Nogo receptor; NgR1; NogoR; NgR; Abeta; Alzheimer's disease;  
 KW neuroprotective; vaccine; gene therapy; human.  
 XX  
 OS Homo sapiens.

# SCORE Search Results Details for Application 10553669 and Search Result 20071121\_092707\_us-10-553-669-4.rag.

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DM protein - protein search, using sw model

Run on: November 21, 2007, 09:27:44 ; Search time 112 Seconds  
(without alignments)  
1393.680 Million cell updates/sec

Title: US-10-553-669-4  
Perfect score: 1711  
Sequence: 1 PCPGACVCYNEPKVTTSCPQ.....TDEEPLGLPKCCQPDAAADKA 319

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2782304 seqs, 489333398 residues

Total number of hits satisfying chosen parameters: 2782304

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_200701:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*  
9: geneseqp2005s:\*  
10: geneseqp2006s:\*  
11: geneseqp2007s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	%	Query			
No.	Score	Match Length	DB	ID	Description

1	1711	100.0	319	8	ADU21104	Adu21104	Human	Nog
2	1711	100.0	319	9	AEB19606	Aeb19606	Human	sol
3	1711	100.0	319	9	AEB86600	Aeb86600	Human	NOG
4	1711	100.0	344	8	ADM33974	Adm33974	Human	Nog
5	1711	100.0	344	8	ADU21101	Adu21101	Human	Nog
6	1711	100.0	344	9	ADY34440	Ady34440	Human	Nog
7	1711	100.0	344	9	AEB19597	Aeb19597	Human	Nog
8	1711	100.0	344	9	AEB86619	Aeb86619	Human	NOG
9	1711	100.0	472	3	AAB33426	Aab33426	Human	PRO
10	1711	100.0	473	2	AAy41745	Aay41745	Human	PRO
11	1711	100.0	473	3	AAB44301	Aab44301	Human	PRO
12	1711	100.0	473	3	AAB24410	Aab24410	Human	PRO
13	1711	100.0	473	3	AAy95345	Aay95345	Human	PRO
14	1711	100.0	473	4	AAU12362	Aau12362	Human	PRO
15	1711	100.0	473	4	AAU04589	Aau04589	Human	Nog
16	1711	100.0	473	4	AAB49891	Aab49891	Human	PRO
17	1711	100.0	473	4	AAB50908	Aab50908	Human	PRO
18	1711	100.0	473	5	AAU83655	Aau83655	Human	PRO
19	1711	100.0	473	5	AAO21479	Aao21479	Human	NgR
20	1711	100.0	473	5	ABB81081	Abb81081	Human	Nog
21	1711	100.0	473	5	ADY31868	Ady31868	Novel	hum
22	1711	100.0	473	6	ABO17806	Abo17806	Novel	hum
23	1711	100.0	473	6	ABU80802	Abu80802	Human	PRO
24	1711	100.0	473	6	ABO25247	Abo25247	Novel	hum
25	1711	100.0	473	6	ABO33768	Abo33768	Novel	hum
26	1711	100.0	473	6	ABU81060	Abu81060	Human	PRO
27	1711	100.0	473	6	ABU72253	Abu72253	Novel	hum
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30	1711	100.0	473	6	ABU59841	Abu59841	Novel	sec
31	1711	100.0	473	6	ABU61131	Abu61131	Human	PRO
32	1711	100.0	473	6	ABO25031	Abo25031	Human	sec
33	1711	100.0	473	6	ABU80400	Abu80400	Human	sec
34	1711	100.0	473	6	ABU82111	Abu82111	Novel	hum
35	1711	100.0	473	6	ABU67036	Abu67036	Human	sec
36	1711	100.0	473	6	ABR59665	Abr59665	Human	Nog
37	1711	100.0	473	6	ADA45901	Ada45901	Novel	hum
38	1711	100.0	473	6	ADA76332	Ada76332	Human	PRO
39	1711	100.0	473	6	ABJ72291	Abj72291	Human	PRO
40	1711	100.0	473	6	ADA18982	Ada18982	Human	PRO
41	1711	100.0	473	6	ADA61605	Ada61605	Homo sapi	
42	1711	100.0	473	6	ADB19390	Adb19390	Novel	hum
43	1711	100.0	473	6	ADB27931	Adb27931	Human	PRO
44	1711	100.0	473	6	ADA86410	Ada86410	Novel	hum
45	1711	100.0	473	6	ADB15974	Adb15974	Human	PRO

## ALIGNMENTS

RESULT 1  
ADU21104

ID ADU21104 standard; protein; 319 AA.

XX

AC ADU21104;

XX

DT 27-JAN-2005 (first entry)

XX

DE Human Nogo receptor NgR1 polypeptide fragment ( residues 26-344).

XX

KW Nogo receptor; NgR1; NogoR; NgR; Abeta; Alzheimer's disease;  
KW neuroprotective; vaccine; gene therapy; human.

XX

OS Homo sapiens.



# SCORE Search Results Details for Application 10553669 and Search Result 20071121\_092707\_us-10-553-669-5.rag.

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OM protein - protein search, using sw model

Run on: November 21, 2007, 09:27:44 ; Search time 100 Seconds  
(without alignments)  
1393.680 Million cell updates/sec

Title: US-10-553-669-5  
Perfect score: 1511  
Sequence: 1 CPGACVCYNPKVTTSRPQQ.....QRLAGRDLKRLATSDLEGCA 284

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2782304 seqs, 489333398 residues

Total number of hits satisfying chosen parameters: 2782304

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_200701:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*  
9: geneseqp2005s:\*  
10: geneseqp2006s:\*  
11: geneseqp2007s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	%	Query				
No.	Score	Match Length	DB	ID		Description

1	1511	100.0	284	8	ADU21105	Adu21105	Rat	Nogo
2	1511	100.0	284	9	AEB19609	Aeb19609	Rat	solub
3	1511	100.0	284	9	AEB86601	Aeb86601	Rat	NOGO
4	1511	100.0	310	8	ADM33977	Adm33977	Rat	Nogo
5	1511	100.0	310	9	ADY34443	Ady34443	Rat	Nogo
6	1511	100.0	310	9	AEB19600	Aeb19600	Rat	Nogo
7	1511	100.0	318	8	ADU21106	Adu21106	Rat	Nogo
8	1511	100.0	318	9	AEB86602	Aeb86602	Rat	NOGO
9	1511	100.0	319	9	AEB19608	Aeb19608	Rat	solub
10	1511	100.0	344	8	ADM33976	Adm33976	Rat	Nogo
11	1511	100.0	344	8	ADU21102	Adu21102	Rat	Nogo
12	1511	100.0	344	9	ADY34442	Ady34442	Rat	Nogo
13	1511	100.0	344	9	AEB19599	Aeb19599	Rat	Nogo
14	1511	100.0	345	9	AEB86620	Aeb86620	Rat	NOGO
15	1489	98.5	471	10	AEH43954	Aeh43954	Rat	Ngr-1
16	1481	98.0	420	8	ADT77798	Adt77798	Chimeric	
17	1481	98.0	441	8	ADT77804	Adt77804	Chimeric	
18	1481	98.0	452	8	ADT77806	Adt77806	Chimeric	
19	1481	98.0	473	8	ADT77786	Adt77786	Rat	Nogo
20	1444	95.6	423	4	AAB87116	Aab87116	Mouse	TAN
21	1444	95.6	447	4	AAB87104	Aab87104	Mouse	mat
22	1444	95.6	473	4	AAB87167	Aab87167	Mouse	sec
23	1444	95.6	473	4	AAB87166	Aab87166	Mouse	sec
24	1444	95.6	473	4	AAB87102	Aab87102	Mouse	sec
25	1444	95.6	473	4	AAU04590	Aau04590	Mouse	Nog
26	1444	95.6	473	5	AAO21488	Aao21488	Mouse	NgR
27	1444	95.6	473	5	AAE26454	Aae26454	Mouse	TAN
28	1444	95.6	473	5	ABB81082	Abb81082	Mouse	Nog
29	1444	95.6	473	6	ABR59666	Abr59666	Murine	No
30	1444	95.6	473	8	ADG75447	Adg75447	Mouse	NoG
31	1444	95.6	473	9	AEB19596	Aeb19596	Soluble	N
32	1444	95.6	473	10	AEK91090	Aek91090	Mouse	TAN
33	1441	95.4	473	4	AAB87169	Aab87169	Mouse	sec
34	1440	95.3	473	4	AAB87168	Aab87168	Mouse	sec
35	1352	89.5	473	8	ADG75446	Adg75446	Macaque	b
36	1351	89.4	285	8	ADU21103	Adu21103	Human	Nog
37	1351	89.4	285	9	AEB19607	Aeb19607	Human	sol
38	1351	89.4	285	9	AEB86599	Aeb86599	Human	NOG
39	1351	89.4	310	8	ADM33975	Adm33975	Human	Nog
40	1351	89.4	310	9	ADY34441	Ady34441	Human	Nog
41	1351	89.4	310	9	AEB19598	Aeb19598	Human	Nog
42	1351	89.4	319	8	ADU21104	Adu21104	Human	Nog
43	1351	89.4	319	9	AEB19606	Aeb19606	Human	sol
44	1351	89.4	319	9	AEB86600	Aeb86600	Human	NOG
45	1351	89.4	344	8	ADM33974	Adm33974	Human	Nog

## ALIGNMENTS

## RESULT 1

ADU21105

ID ADU21105 standard; protein; 284 AA.

XX

AC ADU21105;

XX

DT 27-JAN-2005 (first entry)

XX

DE Rat Nogo receptor NgR1 polypeptide fragment ( residues 27-310).

XX

KW Nogo receptor; NgR1; NogoR; NgR; Abeta; Alzheimer's disease;

KW neuroprotective; vaccine; gene therapy; rat.

XX

OS Rattus sp.

# SCORE Search Results Details for Application 10553669 and Search Result 20071121\_092707\_us-10-553-669-6.rag.

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OM protein - protein search, using sw model

Run on: November 21, 2007, 09:27:44 ; Search time 112 Seconds  
(without alignments)  
1393.680 Million cell updates/sec

Title: US-10-553-669-6  
Perfect score: 1695  
Sequence: 1 CPGACVCYNPKVTTSRPQQ.....TDEELLGLPKCCQPDAAADKA 318

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2782304 seqs, 489333398 residues

Total number of hits satisfying chosen parameters: 2782304

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_200701:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*  
9: geneseqp2005s:\*  
10: geneseqp2006s:\*  
11: geneseqp2007s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
------------	-------	-------	--------	----	----	-------------

1	1695	100.0	318	8	ADU21106	Adu21106	Rat	Nogo
2	1695	100.0	318	9	AEB86602	Aeb86602	Rat	NOGO
3	1695	100.0	319	9	AEB19608	Aeb19608	Rat	solub
4	1695	100.0	344	8	ADM33976	Adm33976	Rat	Nogo
5	1695	100.0	344	8	ADU21102	Adu21102	Rat	Nogo
6	1695	100.0	344	9	ADY34442	Ady34442	Rat	Nogo
7	1695	100.0	344	9	AEB19599	Aeb19599	Rat	Nogo
8	1695	100.0	345	9	AEB86620	Aeb86620	Rat	NOGO
9	1673	98.7	471	10	AEH43954	Aeh43954	Rat	Ngr-1
10	1665	98.2	441	8	ADT77804	Adt77804	Chimeric	
11	1665	98.2	473	8	ADT77786	Adt77786	Rat	Nogo
12	1611	95.0	423	4	AAB87116	Aab87116	Mouse	TAN
13	1611	95.0	447	4	AAB87104	Aab87104	Mouse	mat
14	1611	95.0	473	4	AAB87167	Aab87167	Mouse	sec
15	1611	95.0	473	4	AAB87166	Aab87166	Mouse	sec
16	1611	95.0	473	4	AAB87102	Aab87102	Mouse	sec
17	1611	95.0	473	4	AAU04590	Aau04590	Mouse	Nog
18	1611	95.0	473	5	AAO21488	Aao21488	Mouse	NgR
19	1611	95.0	473	5	AAE26454	Aae26454	Mouse	TAN
20	1611	95.0	473	5	ABB81082	Abb81082	Mouse	Nog
21	1611	95.0	473	6	ABR59666	Abr59666	Murine	No
22	1611	95.0	473	8	ADG75447	Adg75447	Mouse	NOG
23	1611	95.0	473	9	AEB19596	Aeb19596	Soluble	N
24	1611	95.0	473	10	AEK91090	Aek91090	Mouse	TAN
25	1608	94.9	473	4	AAB87169	Aab87169	Mouse	sec
26	1607	94.8	473	4	AAB87168	Aab87168	Mouse	sec
27	1511	89.1	284	8	ADU21105	Adu21105	Rat	Nogo
28	1511	89.1	284	9	AEB19609	Aeb19609	Rat	solub
29	1511	89.1	284	9	AEB86601	Aeb86601	Rat	NOGO
30	1511	89.1	310	8	ADM33977	Adm33977	Rat	Nogo
31	1511	89.1	310	9	ADY34443	Ady34443	Rat	Nogo
32	1511	89.1	310	9	AEB19600	Aeb19600	Rat	Nogo
33	1507	88.9	420	8	ADT77798	Adt77798	Chimeric	
34	1507	88.9	452	8	ADT77806	Adt77806	Chimeric	
35	1492	88.0	473	8	ADG75446	Adg75446	Macaque	b
36	1489	87.8	319	8	ADU21104	Adu21104	Human	Nog
37	1489	87.8	319	9	AEB19606	Aeb19606	Human	sol
38	1489	87.8	319	9	AEB86600	Aeb86600	Human	NOG
39	1489	87.8	344	8	ADM33974	Adm33974	Human	Nog
40	1489	87.8	344	8	ADU21101	Adu21101	Human	Nog
41	1489	87.8	344	9	ADY34440	Ady34440	Human	Nog
42	1489	87.8	344	9	AEB19597	Aeb19597	Human	Nog
43	1489	87.8	344	9	AEB86619	Aeb86619	Human	NOG
44	1489	87.8	472	3	AAB33426	Aab33426	Human	PRO
45	1489	87.8	473	2	AAY41745	Aay41745	Human	PRO

## ALIGNMENTS

RESULT 1  
ADU21106

ID ADU21106 standard; protein; 318 AA.

XX

AC ADU21106;

XX

DT 27-JAN-2005 (first entry)

XX

DE Rat Nogo receptor NgR1 polypeptide fragment ( residues 27-344).

XX

KW Nogo receptor; NgR1; NogoR; NgR; Abeta; Alzheimer's disease;  
KW neuroprotective; vaccine; gene therapy; rat.

XX

OS Rattus sp.

# SCORE Search Results Details for Application 10553669 and Search Result 20071121\_092710\_us-10-553-669-1.rup.

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OM protein - protein search, using sw model

Run on: November 21, 2007, 09:27:44 ; Search time 161 Seconds  
(without alignments)  
2284.144 Million cell updates/sec

Title: US-10-553-669-1  
Perfect score: 1842  
Sequence: 1 MKRASAGGSRLLAWLWLQA.....TDEEPLGLPKCCQPDAAADKA 344

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 3281787 seqs, 1072124677 residues

Total number of hits satisfying chosen parameters: 3281787

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_8.4:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1842	100.0	473	1	RTN4R_HUMAN	Q9bzb6 homo sapien
2	1797	97.6	473	1	RTN4R_MACFA	Q9n0e3 macaca fasc
3	1651	89.6	473	1	RTN4R_MOUSE	Q99pi8 mus musculu
4	1649	89.5	473	1	RTN4R_RAT	Q99m75 rattus norv
5	962.5	52.3	479	2	Q6DH76_BRARE	Q6dh76 brachydanio
6	959.5	52.1	479	2	Q6X3Y5_BRARE	Q6x3y5 brachydanio
7	785.5	42.6	420	1	R4RL2_HUMAN	Q86un3 homo sapien
8	785.5	42.6	420	2	Q17RL9_HUMAN	Q17rl9 homo sapien

9	778.5	42.3	478	2	Q6WZD2_BRARE	Q6wzd2 brachydanio
10	776	42.1	420	1	R4RL2_MOUSE	Q7m6z0 mus musculu
11	775.5	42.1	412	2	Q4RRU8_TETNG	Q4rru8 tetraodon n
12	775.5	42.1	457	2	Q6WZD1_BRARE	Q6wzd1 brachydanio
13	773	42.0	420	1	R4RL2_RAT	Q80wd1 rattus norv
14	772	41.9	441	1	R4RL1_HUMAN	Q86un2 homo sapien
15	760	41.3	445	1	R4RL1_MOUSE	Q8k0s5 mus musculu
16	756	41.0	445	1	R4RL1_RAT	Q80wd0 rattus norv
17	749.5	40.7	310	2	Q4RRQ4_TETNG	Q4rrq4 tetraodon n
18	720.5	39.1	324	2	Q4S3K9_TETNG	Q4s3k9 tetraodon n
19	716	38.9	411	2	Q4S6L6_TETNG	Q4s6l6 tetraodon n
20	691.5	37.5	458	2	Q6WZD3_BRARE	Q6wzd3 brachydanio
21	382	20.7	762	2	Q5JY13_HUMAN	Q5jy13 homo sapien
22	382	20.7	778	2	Q6NUI6_HUMAN	Q6nui6 homo sapien
23	381	20.7	466	2	Q66IW3_XENLA	Q66iw3 xenopus lae
24	376	20.4	411	2	Q4S9P3_TETNG	Q4s9p3 tetraodon n
25	375.5	20.4	481	1	NYX_HUMAN	Q9gzu5 homo sapien
26	375.5	20.4	481	2	Q2M1S4_HUMAN	Q2m1s4 homo sapien
27	372.5	20.2	453	2	Q86XY1_HUMAN	Q86xy1 homo sapien
28	371	20.1	692	2	Q4G0S0_HUMAN	Q4g0s0 homo sapien
29	369	20.0	1461	2	Q5VW18_HUMAN	Q5vw18 homo sapien
30	369	20.0	1534	1	SLIT1_HUMAN	Q75093 homo sapien
31	369	20.0	1534	2	Q5VW17_HUMAN	Q5vw17 homo sapien
32	368.5	20.0	417	2	Q6E4J7_PETMA	Q6e4j7 petromyzon
33	367	19.9	1531	1	SLIT1_RAT	Q88279 rattus norv
34	364	19.8	1531	1	SLIT1_MOUSE	Q80tr4 mus musculu
35	362	19.7	935	2	Q4SBT7_TETNG	Q4sbt7 tetraodon n
36	356.5	19.4	513	1	LRC24_HUMAN	Q50lg9 homo sapien
37	356	19.3	652	2	Q45R42_RAT	Q45r42 rattus norv
38	354	19.2	339	2	Q4SU68_TETNG	Q4su68 tetraodon n
39	354	19.2	652	1	LRRC4_MOUSE	Q99ph1 mus musculu
40	354	19.2	653	1	LRRC4_HUMAN	Q9hbw1 homo sapien
41	354	19.2	782	2	Q5T0V4_HUMAN	Q5t0v4 homo sapien
42	351	19.1	597	2	Q3I0Y3_BOVIN	Q3i0y3 bos taurus
43	351	19.1	602	2	Q58CS0_BOVIN	Q58cs0 bos taurus
44	351	19.1	606	2	Q1KS52_PIG	Q1ks52 sus scrofa
45	351	19.1	640	2	Q4JIW0_HUMAN	Q4jiw0 homo sapien

## ALIGNMENTS

## RESULT 1

## RTN4R\_HUMAN

ID RTN4R\_HUMAN STANDARD; PRT; 473 AA.  
AC Q9BZR6;  
DT 25-NOV-2002, integrated into UniProtKB/Swiss-Prot.  
DT 01-JUN-2001, sequence version 1.  
DT 27-JUN-2006, entry version 54.  
DE Reticulon-4 receptor precursor (Nogo receptor) (NgR) (Nogo-66  
DE receptor).  
GN Name=RTN4R; Synonyms=NOGOR; ORFNames=UNQ330/PRO526;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;  
OC Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [MRNA].  
RC TISSUE=Brain;  
RX MEDLINE=21069055; PubMed=11201742; DOI=10.1038/35053072;  
RA Fournier A.E., GrandPre T., Strittmatter S.M.;  
RT "Identification of a receptor mediating Nogo-66 inhibition of axonal  
RT regeneration."  
RL Nature 409:341-346(2001).

# SCORE Search Results Details for Application 10553669 and Search Result 20071121\_092710\_us-10-553-669-2.rup.

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OM protein - protein search, using sw model

Run on: November 21, 2007, 09:27:44 ; Search time 161 Seconds  
(without alignments)  
2284.144 Million cell updates/sec

Title: US-10-553-669-2  
Perfect score: 1838  
Sequence: 1 MKRASSGG SRLPTWVLWLQA.....TDEELLGLPKCCQPDAAADKA 344

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 3281787 seqs, 1072124677 residues

Total number of hits satisfying chosen parameters: 3281787

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_8.4:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1793	97.6	473	1 RTN4R_RAT	Q99m75 rattus norv
2	1739	94.6	473	1 RTN4R_MOUSE	Q99pi8 mus musculu
3	1612	87.7	473	1 RTN4R_MACFA	Q9n0e3 macaca fasc
4	1605	87.3	473	1 RTN4R_HUMAN	Q9bZR6 homo sapien
5	956.5	52.0	479	2 Q6DH76_BRARE	Q6dh76 brachydanio
6	953.5	51.9	479	2 Q6X3Y5_BRARE	Q6x3y5 brachydanio
7	747	40.6	457	2 Q6WZD1_BRARE	Q6wzd1 brachydanio
8	745.5	40.6	420	1 R4RL2_HUMAN	Q86un3 homo sapien

9	745.5	40.6	420	2	Q17RL9_HUMAN	Q17rl9 homo sapien
10	737.5	40.1	412	2	Q4RRU8_TETNG	Q4rru8 tetraodon n
11	737	40.1	441	1	R4RL1_HUMAN	Q86un2 homo sapien
12	732.5	39.9	478	2	Q6WZD2_BRARE	Q6wzd2 brachydanio
13	730	39.7	445	1	R4RL1_MOUSE	Q8k0s5 mus musculu
14	729.5	39.7	420	1	R4RL2_MOUSE	Q7m6z0 mus musculu
15	724.5	39.4	420	1	R4RL2_RAT	Q80wd1 rattus norv
16	724	39.4	445	1	R4RL1_RAT	Q80wd0 rattus norv
17	714.5	38.9	310	2	Q4RRQ4_TETNG	Q4rrq4 tetraodon n
18	692	37.6	324	2	Q4S3K9_TETNG	Q4s3k9 tetraodon n
19	685	37.3	411	2	Q4S6L6_TETNG	Q4s6l6 tetraodon n
20	649.5	35.3	458	2	Q6WZD3_BRARE	Q6wzd3 brachydanio
21	372.5	20.3	652	2	Q45R42_RAT	Q45r42 rattus norv
22	370	20.1	1461	2	Q5VW18_HUMAN	Q5vw18 homo sapien
23	370	20.1	1534	1	SLIT1_HUMAN	O75093 homo sapien
24	370	20.1	1534	2	Q5VW17_HUMAN	Q5vw17 homo sapien
25	369	20.1	1531	1	SLIT1_RAT	O88279 rattus norv
26	367.5	20.0	652	1	LRRC4_MOUSE	Q99ph1 mus musculu
27	366	19.9	1531	1	SLIT1_MOUSE	Q80tr4 mus musculu
28	365	19.9	653	1	LRRC4_HUMAN	Q9hbw1 homo sapien
29	365	19.9	762	2	Q5JY13_HUMAN	Q5jy13 homo sapien
30	365	19.9	778	2	Q6NUI6_HUMAN	Q6nui6 homo sapien
31	364	19.8	597	2	Q3I0Y3_BOVIN	Q3i0y3 bos taurus
32	364	19.8	602	2	Q58CS0_BOVIN	Q58cs0 bos taurus
33	362	19.7	782	2	Q5T0V4_HUMAN	Q5t0v4 homo sapien
34	359	19.5	1529	2	Q7ZXI2_XENLA	Q7zxi2 xenopus lae
35	357	19.4	692	2	Q4G0S0_HUMAN	Q4g0s0 homo sapien
36	357	19.4	935	2	Q4SBT7_TETNG	Q4sbt7 tetraodon n
37	356	19.4	411	2	Q4S9P3_TETNG	Q4s9p3 tetraodon n
38	355	19.3	466	2	Q66IW3_XENLA	Q66iw3 xenopus lae
39	353	19.2	709	1	LRC4B_MOUSE	P0c192 mus musculu
40	349	19.0	713	1	LRC4B_HUMAN	Q9nt99 homo sapien
41	347	18.9	481	1	NYX_HUMAN	Q9gzu5 homo sapien
42	347	18.9	481	2	Q2M1S4_HUMAN	Q2m1s4 homo sapien
43	344.5	18.7	417	2	Q6E4J7_PETMA	Q6e4j7 petromyzon
44	339.5	18.5	640	2	Q4JIW0_HUMAN	Q4jiw0 homo sapien
45	337.5	18.4	640	1	NGL1_HUMAN	Q9hcj2 homo sapien

## ALIGNMENTS

## RESULT 1

## RTN4R\_RAT

ID RTN4R\_RAT STANDARD; PRT; 473 AA.  
AC Q99M75;  
DT 25-NOV-2002, integrated into UniProtKB/Swiss-Prot.  
DT 10-MAY-2005, sequence version 2.  
DT 27-JUN-2006, entry version 41.  
DE Reticulon-4 receptor precursor (Nogo receptor) (NgR) (Nogo-66  
DE receptor).  
GN Name=Rtn4r; Synonyms=Nogor;  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muroidea; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [MRNA].  
RC STRAIN=Sprague-Dawley;  
RA Jin W.-L., Jia W., Long M., Ju G.;  
RT "Identification and preparation of polyclonal antibody against rat  
RT Nogo receptor."  
RL Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.  
RN [2]



# SCORE Search Results Details for Application 10553669 and Search Result 20071121\_092710\_us-10-553-669-3.rup.

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This page gives you Search Results detail for the Application 10553669 and Search Result 20071121\_092710\_us-10-553-669-3.rup.

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GenCore version 6.2.1  
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3M protein - protein search, using sw model

Run on: November 21, 2007, 09:27:44 ; Search time 134 Seconds  
(without alignments)  
2284.144 Million cell updates/sec

Title: US-10-553-669-3  
Perfect score: 1515  
Sequence: 1 PCPGACVCYNEPKVTTSCPQ.....QRLAGRDLKRLAANDLQGCA 285

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 3281787 seqs, 1072124677 residues

Total number of hits satisfying chosen parameters: 3281787

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_8.4:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1515	100.0	473	1	RTN4R_HUMAN	Q9b2r6 homo sapien
2	1493	98.5	473	1	RTN4R_MACFA	Q9n0e3 macaca fasc
3	1395	92.1	473	1	RTN4R_MOUSE	Q99pi8 mus musculu
4	1391	91.8	473	1	RTN4R_RAT	Q99m75 rattus norv
5	910	60.1	479	2	Q6DH76_BRARE	Q6dh76 brachydanio
6	910	60.1	479	2	Q6X3Y5_BRARE	Q6x3y5 brachydanio
7	774.5	51.1	412	2	Q4RRU8_TETNG	Q4rru8 tetraodon n
8	773.5	51.1	478	2	Q6WZD2_BRARE	Q6wzd2 brachydanio

9	771.5	50.9	420	1	R4RL2_MOUSE	Q7m6z0	mus musculu
10	770.5	50.9	420	1	R4RL2_HUMAN	Q86un3	homo sapien
11	770.5	50.9	420	2	Q17RL9_HUMAN	Q17rl9	homo sapien
12	768.5	50.7	420	1	R4RL2_RAT	Q80wd1	rattus norv
13	761.5	50.3	441	1	R4RL1_HUMAN	Q86un2	homo sapien
14	755.5	49.9	457	2	Q6WZD1_BRARE	Q6wzd1	brachydanio
15	749.5	49.5	310	2	Q4RRQ4_TETNG	Q4rrq4	tetraodon n
16	748.5	49.4	445	1	R4RL1_MOUSE	Q8k0s5	mus musculu
17	745.5	49.2	445	1	R4RL1_RAT	Q80wd0	rattus norv
18	705	46.5	324	2	Q4S3K9_TETNG	Q4s3k9	tetraodon n
19	691.5	45.6	411	2	Q4S6L6_TETNG	Q4s6l6	tetraodon n
20	672.5	44.4	458	2	Q6WZD3_BRARE	Q6wzd3	brachydanio
21	373	24.6	466	2	Q66IW3_XENLA	Q66iw3	xenopus lae
22	372	24.6	411	2	Q4S9P3_TETNG	Q4s9p3	tetraodon n
23	371.5	24.5	762	2	Q5JY13_HUMAN	Q5jy13	homo sapien
24	371.5	24.5	778	2	Q6NUI6_HUMAN	Q6nui6	homo sapien
25	364.5	24.1	692	2	Q4G0S0_HUMAN	Q4g0s0	homo sapien
26	362.5	23.9	481	1	NYX_HUMAN	Q9gzu5	homo sapien
27	362.5	23.9	481	2	Q2MLS4_HUMAN	Q2mls4	homo sapien
28	358.5	23.7	453	2	Q86XY1_HUMAN	Q86xy1	homo sapien
29	354	23.4	935	2	Q4SBT7_TETNG	Q4sbt7	tetraodon n
30	352	23.2	339	2	Q4SU68_TETNG	Q4su68	tetraodon n
31	352	23.2	417	2	Q6E4J7_PETMA	Q6e4j7	petromyzon
32	351.5	23.2	652	2	Q45R42_RAT	Q45r42	rattus norv
33	351	23.2	606	2	Q1KS52_PIG	Q1ks52	sus scrofa
34	349.5	23.1	476	1	NYX_MOUSE	P83503	mus musculu
35	349.5	23.1	652	1	LRRC4_MOUSE	Q99ph1	mus musculu
36	349.5	23.1	653	1	LRRC4_HUMAN	Q9hbw1	homo sapien
37	346.5	22.9	597	2	Q3IBY3_BOVIN	Q3i0y3	bos taurus
38	346.5	22.9	602	2	Q58CS0_BOVIN	Q58cs0	bos taurus
39	345.5	22.8	640	2	Q4JIW0_HUMAN	Q4jiw0	homo sapien
40	343.5	22.7	605	2	Q8TAY0_HUMAN	Q8tay0	homo sapien
41	343.5	22.7	640	1	NGL1_HUMAN	Q9hcj2	homo sapien
42	343.5	22.7	640	1	NGL1_MOUSE	Q8c031	mus musculu
43	343.5	22.7	640	2	Q505E5_MOUSE	Q505e5	mus musculu
44	342.5	22.6	605	1	ALS_HUMAN	P35858	homo sapien
45	341.5	22.5	368	2	Q32QP3_EPTST	Q32qp3	eptatretus

## ALIGNMENTS

## RESULT 1

## RTN4R\_HUMAN

ID RTN4R\_HUMAN STANDARD; PRT; 473 AA.  
AC Q9BZR6;  
DT 25-NOV-2002, integrated into UniProtKB/Swiss-Prot.  
DT 01-JUN-2001, sequence version 1.  
DT 27-JUN-2006, entry version 54.  
DE Reticulon-4 receptor precursor (Nogo receptor) (NgR) (Nogo-66  
DE receptor).  
GN Name=RTN4R; Synonyms=NOGOR; ORFNames=UNQ330/PRO526;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;  
OC Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [MRNA].  
RC TISSUE=Brain;  
RX MEDLINE=21069055; PubMed=11201742; DOI=10.1038/35053072;  
RA Fournier A.E., GrandPre T., Strittmatter S.M.;  
RT "Identification of a receptor mediating Nogo-66 inhibition of axonal  
RT regeneration."  
RL Nature 409:341-346 (2001).